

5' AAA CCT TCA CCT CTC ATG CTG AAG CTC ACA CCC TTG CCC TCC AAG ATG AAG GTT
M L K L T P L P S K M K V

TCT GCA GCG CTT CTG TGC CTG CTG CTC ATG GCA GCC ACT TTC AAG CCT CAG GGA
S A A L L C L L L M A A T F S P Q G

CTT GCT CAG CCA GAT TCA GTT TCC ATT CCA ATC ACC TGC TGC TTT AAC GTG ATC
L A Q P D S V S I P I T C C F N V I

AAT AGG AAA ATT CCT ATC CAG AGG CTG GAG AGC TAC ACA AGA ATC ACC AAC ATC
N R K I P I Q R L E S Y T R I T N I

CAA TGT CCC AAG GAA GCT GTG ATC TTC AAG ACC AAA CGG GGC AAG GAG GTC TGT
Q C P K E A V I F K T K R G K E V C

GCT GAC CCC AAG GAG AGA TGG GTC AGG GAT TCC ATG AAG CAT CTG GAC CAA ATA
A D P K E R W V R D S M K H L D Q I

TTT CAA AAT CTG AAG CCA TGA GCC TTC ATA CAT GGA CTG AGA GTC AGA GCT TGA
F Q N L K P

AGA AAA GCT TAT TTA TTT TCC CCA ACC TCC CCC AGG TGC AGT GTG ACA TTA TTT

TAT TAT AAC ATC CAC AAA GAG ATT ATT TTT AAA TAA TTT AAA GCA TAA TAT TTC

FIGURE 1A

495 504 513 522 531 540
TTA AAA AGT ATT TAA TTA TAT TTA AGT TGT TGA TGT TTT AAC TCT ATC TGT CAT

549 558 567 576 585 594
ACA TCC TAG TGA ATG TAA AAT GCA AAA TCC TGG TGA TGT GTT TTT TGT TTT TGT

603 612 621 630 639 648
TTT CCT GTG AGC TCA ACT AAG TTC ACG GCC AAA NGT CAT TGT TCT CCC TCC TAC

657 666 675 684 693 702
CNG TNC GTA GTG TTG TGG GGT CCT CCC NTG GAT CAT CAA GGT GAA ACA CTT AGG

711 720 729 738 747 756
TAT TCT TTG GCA ATC AGT GCT CCT GTA AGT CAA ATG TGT GCT TTG TAC TGC TGT

765 774 783 792 801 810
TGT TGA AAT TGA NGT TAC TGT ANA TAA CTA TGG AAT TTT GAA AAA AAA TTT CAA

819 828 837 846 855
AAA GAA AAA NAT ATA TAT AAT TTA AAA CTA AAA AAA AAA AAA AAA A 3'

FIGURE 1B

1	M	L	K	L	T	P	L	P	S	K	M	K	V	S	A	A	L	L	C	L	L	L	M	A	A	T	F	S	P	Q	965517
1	M	W	K	P	M	P	S	P	S	N	M	K	A	S	A	A	L	L	C	L	L	L	T	A	A	A	F	S	P	Q	GI 288397
1	M	-	-	-	-	-	-	-	-	-	-	K	V	S	A	A	L	L	C	L	L	L	I	A	A	T	F	I	P	Q	GI 338809
31	G	L	A	Q	P	D	S	V	S	I	P	I	T	C	C	F	N	V	I	N	R	K	I	P	I	Q	R	L	E	S	965517
31	G	L	A	Q	P	V	G	I	N	T	S	T	T	C	C	Y	R	F	I	N	K	K	I	P	K	Q	R	L	E	S	GI 288397
21	G	L	A	Q	P	D	A	I	N	A	P	V	T	C	C	Y	N	F	T	N	R	K	I	S	V	Q	R	L	A	S	GI 338809
61	Y	T	R	I	T	N	I	Q	C	P	K	E	A	V	I	F	K	T	K	R	G	K	E	V	C	A	D	P	K	E	965517
61	Y	R	R	T	T	S	S	H	C	P	R	E	A	V	I	F	K	T	K	L	D	K	E	I	C	A	D	P	T	Q	GI 288397
51	Y	R	R	I	T	S	S	K	C	P	K	E	A	V	I	F	K	T	I	V	A	K	E	I	C	A	D	P	K	Q	GI 338809
91	R	W	V	R	D	S	M	K	H	L	D	Q	I	F	Q	N	L	K	P	965517											
91	K	W	V	Q	D	F	M	K	H	L	D	K	K	T	Q	T	P	K	L	GI 288397											
81	K	W	V	Q	D	S	M	D	H	L	D	K	Q	T	Q	T	P	K	T	GI 338809											

FIGURE 2

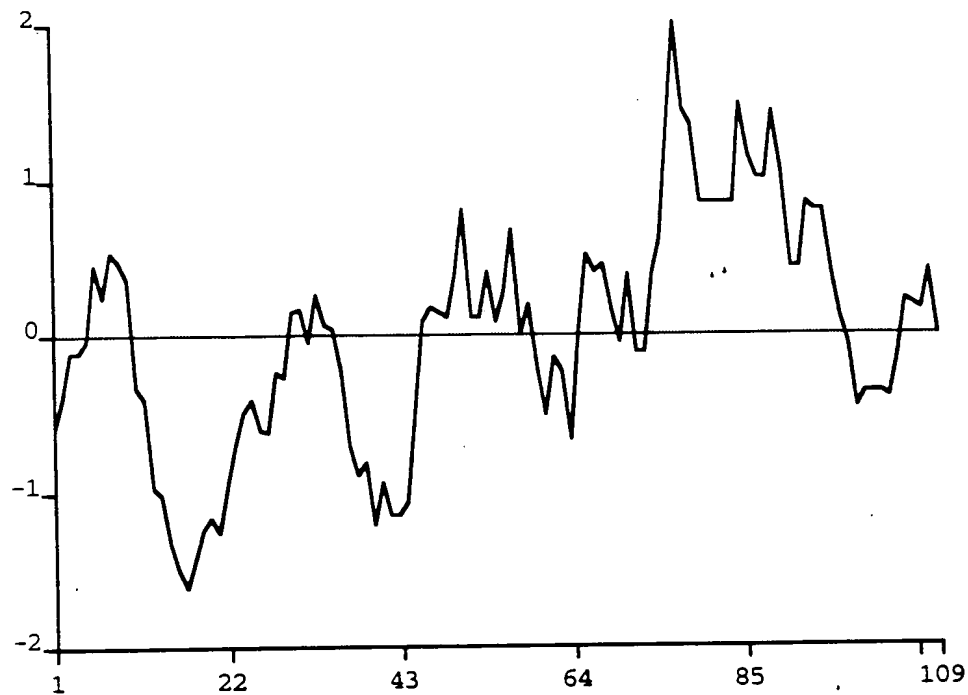


FIGURE 3

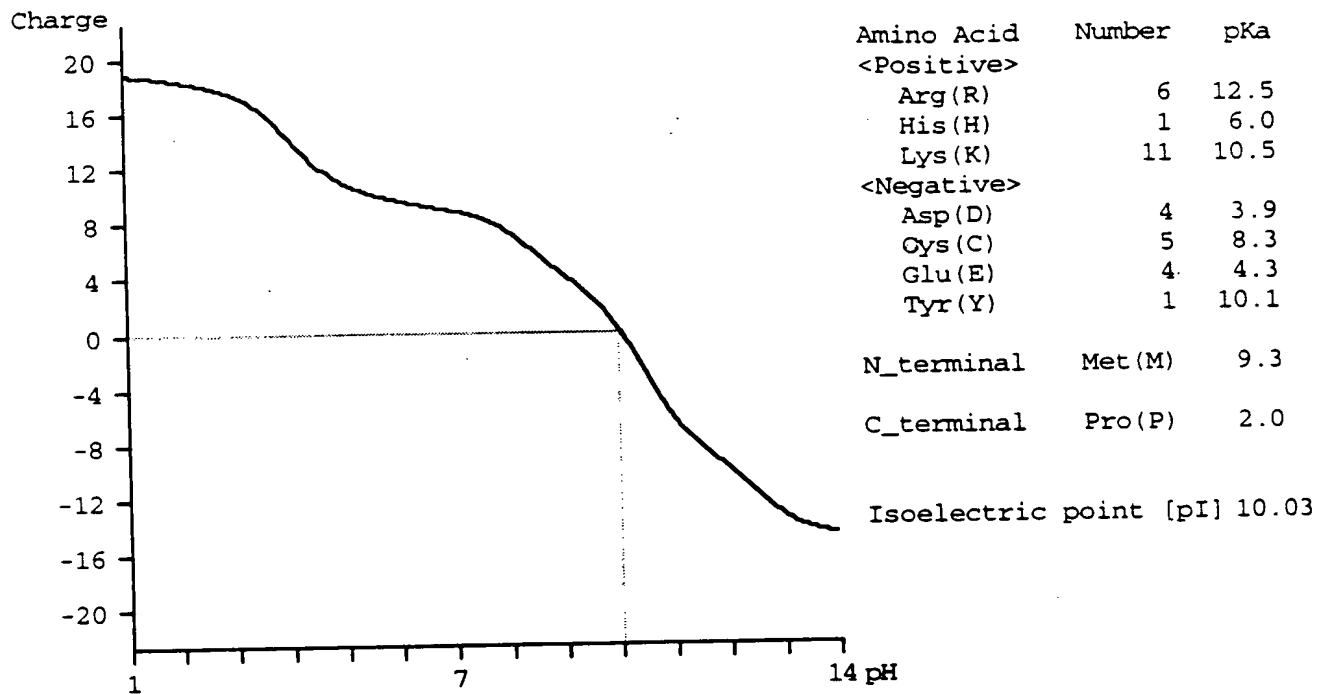


FIGURE 4

The Electronic Northern for Clone: 965517
and Stringency = 50

Library	Lib Description	Abun	Pct	Abur
PANCDIT03	pancreas, NIDDM, 57 M	1		0.145
MMLR1DT01	macrophages (adher PBMNC), M/F, 24-hr MLR	4		0.094
MMLR3DT01	macrophages (adher PBMNC), M/F, 72-hr MLR	2		0.066
MPHGLPT02	macrophages (adher PBMNC), M/F, treated LPS	1		0.045
TMLR3DT01	lymphocytes (non-adher PBMNC), M, 96-hr MLR	2		0.045
BLADTUT02	bladder tumor, carcinoma, 80 F	1		0.030
SYNORAT05	synovium, knee, rheumatoid, 62 F	1		0.028
LUNGNOT01	lung, 72 M, WM	1		0.026
MPHGNOT03	macrophages (adher PBMNC), M/F	2		0.025
BRSTNOT05	breast, 58 F, match to BRSTTUT03	1		0.015

FIGURE 5